GenCore version 6.2
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:33:46 ; Search time 520 Seconds
                                            (without alignments)
                                            304.787 Million cell updates/sec

Title: US-10-529-447-19
Perfect score: 21
Sequence: 1 gcctgcagtttgaaatcagtg 21

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 14153951 seqs, 3772896607 residues

Total number of hits satisfying chosen parameters: 28307902

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   Published_Applications_NA_New:*
        1:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
        2:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
        3:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
        4:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
        5:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
        6:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
        7:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq1:*
        8:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB:seq2:*
        9:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq3:*
        10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq4:*
        11: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq5:*
        12: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq6:*
        13: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
        14: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
        15: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
        16: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
        17: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
        18: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq5:*
        19: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq6:*
        20: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                           SUMMARIES
            %

GenCore version 6.2
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:33:46 ; Search time 470 Seconds
                                            (without alignments)
                                            304.787 Million cell updates/sec

Title: US-10-529-447-20
Perfect score: 19
Sequence: 1 cgggacgggctttagctat 19

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 14153951 seqs, 3772896607 residues

Total number of hits satisfying chosen parameters: 28307902

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   Published_Applications_NA_New:*
                1:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                2:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                3:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                4:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                5:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                6:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                7:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq1:*
                8:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq2:*
                9:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq3:*
                10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq4:*
                11: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq5:*
                12: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq6:*
                13: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
                14: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
                15: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
                16: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
                17: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
                18: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq5:*
                19: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq6:*
                20: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                %

GenCore version 6.2
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:33:46 ; Search time 644 Seconds
                                            (without alignments)
                                            304.787 Million cell updates/sec

Title: US-10-529-447-30
Perfect score: 26
Sequence: 1 tggaagctaatgggaagcccagtacc 26

Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 14153951 seqs, 3772896607 residues

Total number of hits satisfying chosen parameters: 28307902

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   Published_Applications_NA_New:*
                   1:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                   2:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                   3:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                   4:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                   5:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                   6:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                   7:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq1:*
                   8:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq2:*
                   9:   /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq3:*
                   10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq4:*
                   11: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq5:*
                   12: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq6:*
                   13: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
                   14: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
                   15: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
                   16: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
                   17: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
                   18: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq5:*
                   19: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq6:*
                   20: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
            %

GenCore version 6.2
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:23:25 ; Search time 613 Seconds
                                            (without alignments)
                                            420.853 Million cell updates/sec

Title: US-10-529-447-19
Perfect score: 21
Sequence: 1 gcctgcagtttgaaatcagtg 21

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   Published_Applications_NA_Main:*
                 1:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 3:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                 4:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                 5:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                 6:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                 7:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                 8:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                 9:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                 10:. /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
                 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
                 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
                 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
                 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
                 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
   No.   Score Match Length DB   ID   Description
----
     1   21 100.0   2224 6   US-10-027-632-102238   Sequence 102238,

GenCore version 6.2
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:23:25 ; Search time 555 Seconds
                                             (without alignments)
                                             420.853 Million cell updates/sec

Title: US-10-529-447-20
Perfect score: 19
Sequence: 1 cgggacgggctttagctat 19

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   Published_Applications_NA_Main:*
                1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
                12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
                13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
                14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
                15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
                16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
  c   1   19   100.0   2224 6   US-10-027-632-102238   Sequence 102238,

GenCore version 6.2
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:23:25 ; Search time 759 Seconds
                                           (without alignments)
                                           420.853 Million cell updates/sec

Title: US-10-529-447-30
Perfect score: 26
Sequence: 1 tggaagctaatgggaagcccagtacc 26

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   Published_Applications_NA_Main:*
                 1:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 3:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                 4:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                 5:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                 6:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                 7:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
                 8:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                 9:   /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
                 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
                 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
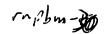   13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
                 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
                 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
                 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                       %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
     1   26   100.0   2224 6   US-10-027-632-102238   Sequence 102238,

GenCore version 6.2
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:18:36 ; Search time 66 Seconds
                                           (without alignments)
                                           596.585 Million cell updates/sec

Title: US-10-529-447-19
Perfect score: 21
Sequence: 1 gcctgcagtttgaaatcagtg 21

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   Issued_Patents_NA:*
                 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
                 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
                 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
                 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
                 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
                 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
                 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
                 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
                 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
                 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	100.0	601	3	US-09-949-016-164991	Sequence 164991,
2	21	100.0	10024	4	US-09-880-107-2430	Sequence 2430, Ap
3	21	100.0	12665	3	US-09-949-016-16388	Sequence 16388, A
4	19.4	92.4	1034	3	US-09-358-856C-7	Sequence 7, Appli
5	19.4	92.4	1034	3	US-09-358-856C-10	Sequence 10, Appl
6	19.4	92.4	1035	3	US-09-358-856C-3	Sequence 3, Appli
7	19.4	92.4	1035	3	US-09-358-856C-5	Sequence 5, Appli

GenCore version 6.2
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:18:36 ; Search time 60 Seconds
                                           (without alignments)
                                           596.585 Million cell updates/sec

Title: US-10-529-447-20
Perfect score: 19
Sequence: 1 cgggacgggctttagctat 19

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   Issued_Patents_NA:*
                1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
                2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
                3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
                4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
                5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
                6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
                7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
                8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
                9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
                10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                     %
Result   Query
    No.   Score   Match Length DB ID   Description
    ----
    c   1   19 100.0   601 3 US-09-949-016-164991   Sequence 164991,
    c   2   19 100.0   601 3 US-09-949-016-164992   Sequence 164992,
    c   3   19 100.0 10024 4 US-09-880-107-2430   Sequence 2430, Ap
    c   4   19 100.0 12665 3 US-09-949-016-16388   Sequence 16388, A
    c   5   15.8   83.2   601 3 US-09-949-016-88349   Sequence 88349, A
    c   6   15.8   83.2   601 3 US-09-949-016-88350   Sequence 88350, A
    c   7   15.8   83.2 36016 3 US-09-949-016-14223   Sequence 14223, A

GenCore version 6.2
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:18:36 ; Search time 82 Seconds
                                            (without alignments)
                                            596.585 Million cell updates/sec

Title: US-10-529-447-30
Perfect score: 26
Sequence: 1 tggaagctaatgggaagcccagtacc 26

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   Issued_Patents_NA:*
                 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
                 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
                 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
                 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
                 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
                 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
                 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
                 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
                 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
                 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                 SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	26	100.0	601	3	US-09-949-016-164991	Sequence 164991,
2	26	100.0	601	3	US-09-949-016-164992	Sequence 164992,
3	26	100.0	10024	4	US-09-880-107-2430	Sequence 2430, Ap
4	26	100.0	12665	3	US-09-949-016-16388	Sequence 16388, A
c 5	18.6	71.5	601	3	US-09-949-016-31506	Sequence 31506, A
c 6	18.6	71.5	601	3	US-09-949-016-31507	Sequence 31507, A
7	18.6	71.5	601	3	US-09-949-016-187176	Sequence 187176,

GenCore version 6.2
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:05:50 ; Search time 2126 Seconds
                                            (without alignments)
                                            612.888 Million cell updates/sec

Title: US-10-529-447-19
Perfect score: 21
Sequence: 1 gcctgcagtttgaaatcagtg 21

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est3:*
                 3: gb_est4:*
                 4: gb_est5:*
                 5: gb_est6:*
                 6: gb_htc:*
                 7: gb_est2:*
                 8: gb_est7:*
                 9: gb_est8:*
                 10: gb_est9:*
                 11: gb_est13:*
                 12: gb_est12:*
                 13: gb_est11:*
                 14: gb_est10:*
                 15: gb_gss1:*
                 16: gb_gss2:*
                 17: gb_gss3:*
                 18: gb_gss4:*
                 19: gb_gss5:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                         %
Result   Query

GenCore version 6.2
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:05:50 ; Search time 1923 Seconds
                                          (without alignments)
                                          612.888 Million cell updates/sec

Title: US-10-529-447-20
Perfect score: 19
Sequence: 1 cgggacgggctttagctat 19

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est3:*
                 3: gb_est4:*
                 4: gb_est5:*
                 5: gb_est6:*
                 6: gb_htc:*
                 7: gb_est2:*
                 8: gb_est7:*
                 9: gb_est8:*
                 10: gb_est9:*
                 11: gb_est13:*
                 12: gb_est12:*
                 13: gb_est11:*
                 14: gb_est10:*
                 15: gb_gss1:*
                 16: gb_gss2:*
                 17: gb_gss3:*
                 18: gb_gss4:*
                 19: gb_gss5:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                     %
Result   Query

GenCore version 6.2
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:05:50 ; Search time 2632 Seconds
                                            (without alignments)
                                            612.888 Million cell updates/sec

Title: US-10-529-447-30
Perfect score: 26
Sequence: 1 tggaagctaatgggaagcccagtacc 26

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est3:*
                 3: gb_est4:*
                 4: gb_est5:*
                 5: gb_est6:*
                 6: gb_htc:*
                 7: gb_est2:*
                 8: gb_est7:*
                 9: gb_est8:*
                 10: gb_est9:*
                 11: gb_est13:*
                 12: gb_est12:*
                 13: gb_est11:*
                 14: gb_est10:*
                 15: gb_gss1:*
                 16: gb_gss2:*
                 17: gb_gss3:*
                 18: gb_gss4:*
                 19: gb_gss5:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                        %
Result   Query

GenCore version 6.2
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:04:22 ; Search time 1042 Seconds
                                           (without alignments)
                                           1392.959 Million cell updates/sec

Title: US-10-529-447-19
Perfect score: 21
Sequence: 1 gcctgcagtttgaaatcagtg 21

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   GenEmbl:*
                 1:   gb_env:*
                 2:   gb_pat:*
                 3:   gb_ph:*
                 4:   gb_pl:*
                 5:   gb_pr:*
                 6:   gb_ro:*
                 7:   gb_sts:*
                 8:   gb_sy:*
                 9:   gb_un:*
                 10: gb_vi:*
                 11: gb_ov:*
                 12: gb_htg:*
                 13: gb_in:*
                 14: gb_om:*
                 15: gb_ba:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
     1   21   100.0   21   2   DD309751   DD309751 Method an
     2   21   100.0   134   5   HSPBGD   X68018 H.sapiens g

GenCore version 6.2
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:04:22 ; Search time 943 Seconds
                                          (without alignments)
                                          1392.959 Million cell updates/sec

Title: US-10-529-447-20
Perfect score: 19
Sequence: 1 cgggacgggctttagctat 19

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   GenEmbl:*
               1: gb_env:*
               2: gb_pat:*
               3: gb_ph:*
               4: gb_pl:*
               5: gb_pr:*
               6: gb_ro:*
               7: gb_sts:*
               8: gb_sy:*
               9: gb_un:*
               10: gb_vi:*
               11: gb_ov:*
               12: gb_htg:*
               13: gb_in:*
               14: gb_om:*
               15: gb_ba:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                                    SUMMARIES
                         %
Result   Query
    No.   Score   Match Length DB   ID   Description
----
      1   19   100.0   19 2   DD309752   DD309752 Method an
c   2   19   100.0 10024 2   AR781867   AR781867 Sequence

GenCore version 6.2
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:04:22 ; Search time 1290 Seconds
                                           (without alignments)
                                           1392.959 Million cell updates/sec

Title: US-10-529-447-30
Perfect score: 26
Sequence: 1 tggaagctaatgggaagcccagtacc 26

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   GenEmbl:*
                 1: gb_env:*
                 2: gb_pat:*
                 3: gb_ph:*
                 4: gb_pl:*
                 5: gb_pr:*
                 6: gb_ro:*
                 7: gb_sts:*
                 8: gb_sy:*
                 9: gb_un:*
                 10: gb_vi:*
                 11: gb_ov:*
                 12: gb_htg:*
                 13: gb_in:*
                 14: gb_om:*
                 15: gb_ba:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
   No.   Score Match Length DB   ID   Description
----
      1   26 100.0   26 2   DD309762   DD309762 Method an
      2   26 100.0 10024 2   AR781867   AR781867 Sequence

GenCore version 6.2
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:03:24 ; Search time 497 Seconds
                                         (without alignments)
                                         387.865 Million cell updates/sec

Title: US-10-529-447-30
Perfect score: 26
Sequence: 1 tggaagctaatgggaagcccagtacc 26

Scoring table: IDENTITY_NUC·
               Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   N_Geneseq_200701:*
               1: geneseqn1980s:*
               2: geneseqn1990s:*
               3: geneseqn2000s:*
               4: geneseqn2001as:*
               5: geneseqn2001bs:*
               6: geneseqn2002as:*
               7: geneseqn2002bs:*
               8: geneseqn2003as:*
               9: geneseqn2003bs:*
               10: geneseqn2003cs:*
               11: geneseqn2003ds:*
               12: geneseqn2004as:*
               13: geneseqn2004bs:*
               14: geneseqn2005s:*
               15: geneseqn2006s:*
               16: geneseqn2007s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                       %
Result   Query
  No.   Score Match Length DB   ID   Description
      ----
      1   26 100.0   26 12 ADM82975   Adm82975 Human pap

GenCore version 6.2
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:03:24 ; Search time 401 Seconds
                                            (without alignments)
                                            387.865 Million cell updates/sec

Title: US-10-529-447-19
Perfect score: 21
Sequence: 1 gcctgcagtttgaaatcagtg 21

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   N_Geneseq_200701:*
             1: geneseqn1980s:*
             2: geneseqn1990s:*
             3: geneseqn2000s:*
             4: geneseqn2001as:*
             5: geneseqn2001bs:*
             6: geneseqn2002as:*
             7: geneseqn2002bs:*
             8: geneseqn2003as:*
             9: geneseqn2003bs:*
             10: geneseqn2003cs:*
             11: geneseqn2003ds:*
             12: geneseqn2004as:*
             13: geneseqn2004bs:*
             14: geneseqn2005s:*
             15: geneseqn2006s:*
             16: geneseqn2007s:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
  No.   Score Match Length DB   ID   Description
----
    1   21   100.0   21 12   ADM82967   Adm82967 Human pap

GenCore version 6.2
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:03:24 ; Search time 363 Seconds
                                            (without alignments)
                                            387.865 Million cell updates/sec

Title: US-10-529-447-20
Perfect score: 19
Sequence: 1 cgggacgggctttagctat 19

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 200 summaries

Database :   N_Geneseq_200701:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*
                 14: geneseqn2005s:*
                 15: geneseqn2006s:*
                 16: geneseqn2007s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query
   No. Score Match Length DB   ID   Description
----
     1   19 100.0   19 12   ADM82968   Adm82968 Human pap